

10                    30                    50  
 CATGGGTGGGGTGGGGCGCTGCTGGATTCTGCTCTGGTGGAGGGAAACTTGTGAGG  
  
 70                    90                    110  
 GGCTGGTAAGCGCCCCCTCCGAAGCCTGGTGTGCGCGGGGGAGGAAAGTTAGTTCC  
  
 130                    150                    170  
 TCTCCACCCATGGGCACCCCTCTGCCCGGGGCTGGGAAGTGCGCTGCTGTGGCAA  
  
 190                    210                    230  
 ATGCTGGGCCTCTGAAATGGAGGGAGACGCAGCAGGGAGAGGCCACGTGGCAGCTGC  
M E E T O O G E A P R G Q L R  
  
 250                    270                    290  
 GCGGAGAGTCAGCAGCACCTGTCCCCAGGCGCTCCTGGTGTGCTGGGGCCCGGG  
G E S A A P V P Q A L L V L L G A R A  
  
 310                    330                    350  
 CCCAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTACTTCCACAAGAAGATTG  
Q G G T R S P R C D C A G D F H K K I G  
  
 370                    390                    410  
 GTCTGTTTGTGCAAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGCACGGAGC  
L F C C R G C P A G H Y L K A P C T E P  
  
 430                    450                    470  
 CCTGCGGCAACTCCACCTGCCTGTGTGTCCTAACCTTGGCCTGGAGAAC  
C G N S T C L V C P Q D T F L A W E N H  
  
 490                    510                    530  
 ACCATAATTCTGAATGTGCCGCTGCCAGGCCTGTGATGAGCAGGCCTCCAGGTGGCGC  
H N S E C A R C Q A C D E Q A S Q V A L  
  
 550                    570                    590  
 TGGAGAACTGTTCAGCAGTGGCCACCCGCTGTGGCTGTAAGCCAGGCTGGTTGTGG  
E N C S A V A D T R C G C K P G W F V E  
  
 610                    630                    650  
 AGTGCCAGGTCAAGCCAATGTGTCAGCAGTTCACCCCTACTGCCAACCATGCCTAGACT  
C Q V S Q C V S S S P F Y C Q P C L D C

**FIG. 1A**

670	690	710
GCGGGGCCCTGCACGCCACACACGGCTACTCTGTTCCGCAGAGATACTGACTGTGGGA		
G A L H R H T R L L C S R R D T D C G T		
730		
CCTGCCTGCCTGGCTTCTATGAACATGGCGATGGCTGCGTCCTGCCAACGAGCACCC		
C L P G F Y E H G D G C V S C P T S T L		
750		
TGGGGAGCTGTCCAGAGCGCTGTGCCGTGCTGTGGCTGGAGGCAGATGTTCTGGTCC		
G S C P E R C A A V C G W R Q M F <u>W</u> V Q		
790		
AGGTGCTCCTGGCTGGCCTTGTGGTCCCCCTCCTGCTGGGCCACCCGTACCATACAT		
<u>V</u> L L A G L V V P <u>L</u> L G A T L T Y T Y		
810		
910		
ACCGCCACTGCTGGCCTCACAAAGCCCCTGGTTACTGCAGATGAAGCTGGGATGGAGGCTC		
R H C W P H K P L V T A D E A G M E A L		
930		
950		
TGACCCCCACCACCGGCCACCCATCTGTCAACCTTGGACAGCGCCCACACCCCTTAGCAC		
T P P P A T H L S P L D S A H T L L A P		
890		
1030		
CTCCTGACAGCAGTGAGAAGATCTGCACCGTCCAGTTGGTGGTAACAGCTGGACCCCTG		
P D S S E K I C T V Q L V G N S W T P G		
1050		
1090		
GCTACCCCGAGACCCAGGAGGGCCTCTGCCCGCAGGTGACATGGCTGGACCAAGTTGC		
Y P E T Q E A L C P Q V T W S W D Q L P		
1110		
1150		
CCAGCAGAGCTTGGCCCCGCTGCTGCAGCCACACTCTGCCAGAGTCCCCAGCCGGCT		
S R A L G P A A A P T L S P E S P A G S		
1170		
1210		
CGCCAGCCATGATGCTGCAGCCGGCCCGCAGCTCTACGACGTGATGGACGCGGTCCAG		
P A M M L Q P G P Q L Y D V M D A <u>V</u> P A		
1190		
1230		
1270		
CGCGCGCTGGAAGGAGTTCGTGCACGCTGGGCTGCGAGGCAGAGATCGAAGCCG		
<u>R</u> R W K E F V R T L G L R E A E I E A V		
1250		
1290		
1310		

**FIG.1B**

1330                    1350                    1370  
TGGAGGTGGAGATCGGCCGCTTCCGAGACCAGCAGTACGAGATGCTCAAGCGCTGGCGCC  
E V E I G R F R D O O Y E M L K R W R Q

1390                    1410                    1430  
AGCAGCAGCCCCGGGCCTCGGAGGCCCTACGCCGCCTGGAGCGCATGGGGCTGGACG  
Q Q P A G L G A V Y A A L E R M G L D G

1450                    1470                    1490  
GCTGCGTGGAAAGACTTGCGCAGCCGCCTGCAGCGCCCGTGACACGGCGCCACTTGC  
C V E D L R S R L Q R G P \*

1510                    1530                    1550  
CACCTAGGCGCTCTGGTGGCCCTTGCAGAAGCCCTAAGTACGGTTACTTATGCGTGTAGA

1570                    1590                    1610  
CATTTTATGTCACTTATTAGCCGCTGGCACGGCCCTGCGTAGCAGCACAGGCCGGCCCC

1630                    1650                    1670  
ACCCCTGCTCGCCCCATCGCTCCAGCCAAGGCCAAGAACGAATGTCGAGAGG

1690                    1710                    1730  
GGGTGAAGACATTCTCAACTTCTCGGCCGGAGTTGGCTGAGATCGCGGTATTAAATCT

1750                    1770  
GTGAAAGAAAACAAACAAACAAAAA

## FIG. 1C

1 ATGGAGCAGC GGCGCCGGGG CTGCGCGGCG GTGGCGCGG CGCTCCTCCT GGTGCTGCTG  
M E Q R P R G C A A V A A A L L L V L L

61 GGGGCCCGGG CCCACGGCGG CACTCGTAGC CCCAGGTGTG ACTGTCCCCG TGACTTCCAC  
G A R A Q G G T R S P R C D C A G D F H

121 AAGAAGATTG GTCTGTTTG TTGCAGAGGC TGCCCAGCGG GCCACTACCT GAAGGCCCC  
K K I G L F C C R G C P A G H Y L K A P

181 TGCACGGAGC CCTGCGGCAA CTCCACCTGC CTTGTGTGTC CCCAAGACAC CTTCTTGGCC  
C T E P C G N S T C L V C P Q D T F L A

241 TGGGAGAAC ACCATAATTG TGAATGTGCC CGCTGCCAGG CCTGTGATGA GCAGGCCCTCC  
W E N H H N S E C A R C Q A C D E Q A S

301 CAGGTGGCGC TGGAGAACTG TTCAGCAGTG GCCGACACCC GCTGTGGCTG TAAGCCAGGC  
Q V A L E N C S A V A D T R C G C K P G

361 TGGTTTGTGG ACTGCCAGGT CAGCCAATGT GTCAGCAGTT CACCCTCTA CTGCCAACCA  
W F V E C Q V S Q C V S S S P F Y C Q P

421 TGCCTAGACT GCGGGGCCCT GCACCGCCAC ACACGGCTAC TCTGTTCCCG CAGAGATACT  
C L D C G A L H R H T R L L C S R R D T

481 GACTGTGGGA CCTGCCTGCC TGGCTTCTAT GAACATGGCG ATGGCTGGGT GTCCCTGCC  
D C G T C L P G F Y E H G D G C V S C P

541 ACGAGCACCC TGGGGAGCTG TCCAGAGCGC TGTGCCGCTG TCTGTGGCTG GAGGCAGATG  
T S T L G S C P E R C A A V C G W R Q M

601 TTCTGGTCC AGGTGCTCCT GGCTGGCCTT GTGGTCCCCC TCCTGCTTGG GGCCACCC  
F W V Q V L L A G L V V P L L L G A T L

661 ACCTACACAT ACCGCCACTG CTGGCCTCAC AAGCCCCCTGG TTACTGCAGA TGAAGCTGGG  
T Y T Y R H C W P H K P L V T A D E A G

721 ATGGAGGCTC TGACCCCCACC ACCGGCCACC CATCTGTAC CCTTGGACAG CGCCACACCC  
M E A L T P P P A T H L S P L D S A H T

781 CTTCTAGCAC CTCCGTACAG CAGTGAGAAC ATCTGCACCG TCCAGTTGGT GCGTAACAGC  
L L A P P D S S E K I C T V Q L V G N S

**FIG.2A**

841 TGGACCCCTG GCTACCCCCA GACCCAGGAG GCGCTCTGCC CGCAGGTGAC ATGGTCTGG  
W T P G Y P E T Q E A L C P Q V T W S W

901 GACCAGTTGC CCAGCAGAGC TCTTGGCCCC GCTGCTGGCC CCACACTCTC GCCAGAGTCC  
D Q L P S R A L G P A A A P T L S P E S

961 CCAGCCCCCT CGCCAGCCAT GATGCTGCAG CCGGGCCCCCG AGCTCTACGA CGTGATGGAC  
P A G S P A M M L Q P G P Q L Y D V M D

1021 CGGGTCCCAG CGCGCCGCTG GAAGGAGTTC GTGCCACCC TGGGCTGCC CGAGGCAGAG  
A V P A R R W K E F V R T L G L R E A E

1081 ATCGAAGCCG TGGAGGTGGA GATCGGCCGC TTCCGAGACC AGCACTACGA GATGCTCAAG  
I E A V E V E I G R F R D Q Q Y E M L K

1141 CGCTGGCGCC AGCAGCAGCC CGCGGCCCTC GGAGCCCTT ACCGGCCCT GGAGCCATG  
R W R Q Q Q P A G L G A V Y A A L E R M

1201 CGGCTGGACG GCTCGTGGAG AGACTTGCAG AGCCGCCCTGC AGCCGGCCCG GTGA  
G L D G C V E D L R S R L Q R G P

FIG.2B

**FIG. 3A**

Consensus #1	.....T.C.C.....	.....C.....	.....C.....	.....C.....	.....C.....	.....C.....	.....C.....	.....C.....	.....C.....
DDCR	SAVAD	TRCCC	KPG	WFE	VEC	-	-	QVS	CVS
TNFR1	TVDRD	TCC	CRK	NQY	RHY	WSEN	LFC	-	-
FAS	RTQNT	TKC	RCK	PNF	QFN	-	-	-	137
Consensus #1	.....C.....	.....C.....	.....C.....	.....C.....	.....C.....	.....C.....	.....C.....	.....C.....	.....C.....
DDCR	PFYCQ	PCPCL	DCGA	LH	RHTR	LC	SRRDT	DCG	175
TNFR1	-FNC	SLC	LN-G	T	VH	-L	SCQ	EQNTV	167
FAS	--	-ST	VCE	HCD	P	--	--	-CTK	148
Consensus #1	C.....C.....	G.....G.....	. . . . .	C.....C.....	. . . . .	C.....C.....	. . . . .	C.....C.....	. . . . .
DDCR	CLPGF	YEHGD	GCVSC	PTSTL	G-	SCP	PERC	C-	203
TNFR1	CHAGF	FLRENE	CVSC	SNC	KK	SL	ECTKL	CLP	197
FAS	CEHGI	I	-	-KEC	-	-T	TSNTKC	-	166
Consensus #1	.....C.....	.....C.....	.....C.....	.....C.....	.....C.....	.....C.....	.....C.....	.....C.....	.....C.....
DDCR	-	-	-	A	AVC	GWQ	VLL	ACLV	225
TNFR1	QIENVKGT	EDSGT	TTV	LLP	VIF	FGLC	LLS	L	227
FAS	--	--	-K	EEG	SRSNL	GWL	CLL	-LPIL	186

FIG. 3B

FIG. 3C

## Consensus #1

EY

DDDCR	Q P G P Q L Y D V M D A V P A R R W K E F V	362
TNFR1	D D P A T L Y A V V E N V P P L R W K E F V	375
FAS	D V D L S K Y I T T I A G V M T L S Q V K G F V	249
---	---	---
H K P Q S L D T	Q P G P Q L Y D V M D A V P A R R W K E F V	362

Consensus #1 R : . G : . . . I : . . .

DDCR	R T L G L R R R	T E A E V E I G R - F R D Q Q Y E M L K	391
TNFR1	R L G L S D H E I D R L E L Q N G R C L R E A Q Y S M L A	E M L K S M L A 405	
FAS	R K N G V N E A K I D E I K N D N V Q D T A E Q K V Q L L R	S M L A 405	279

Consensus #1 - W

DDCR R W R Q Q P - - A G L G A V Y A A L E R M C L D G C C V E 418  
 TNFR1 T W R R T P R R E A T L E L G R V L R D M D L L G C L E 435  
 FAS N W H Q L H G K K E A - Y D T I K D L I C T I A E 308

Concessions #1

DDCR 428  
TNFR1 455  
FAS 335

FIG. 3D

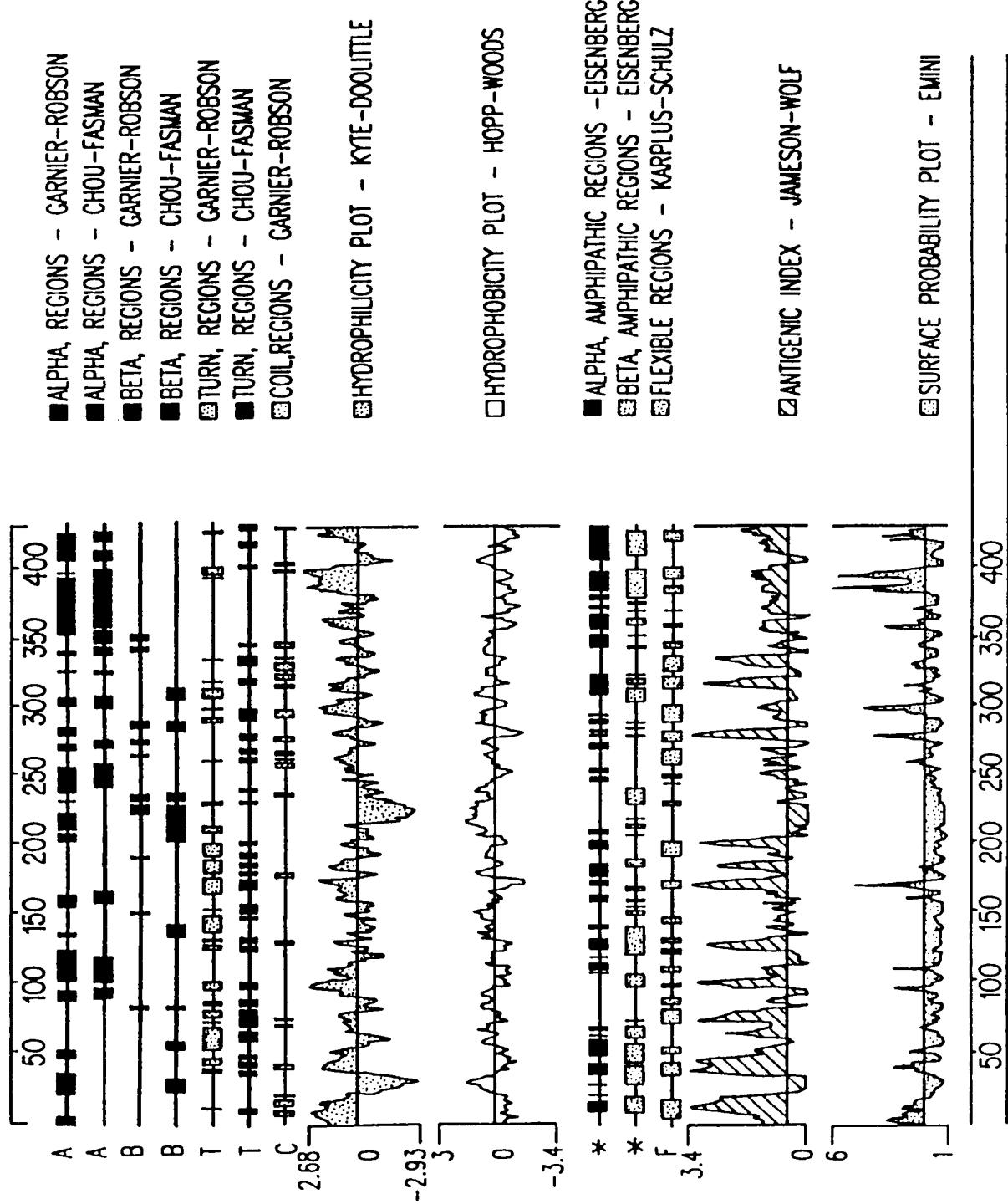


FIG. 4